

Exhibit A

Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/818,990

1. (Amended) An isolated nucleic acid molecule comprising at least 2000 contiguous bases of nucleotide sequence first disclosed in SEQ ID NO: 1.
2. (Twice Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
 - (a) encodes the amino acid sequence shown in SEQ ID NO: 2; and
 - (b) hybridizes to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.
6. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1.
7. A recombinant expression vector comprising the isolated nucleic acid molecule of claim 1.
8. The recombinant expression vector of claim 7, wherein the isolated nucleic acid molecule encodes the amino acid sequence shown in SEQ ID NO:2.
9. The recombinant expression vector of claim 8, wherein the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 1.

10. A host cell comprising the recombinant expression vector of claim 7.

Exhibit B

Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/818,990

1. (Amended) An isolated nucleic acid molecule comprising at least [24] 2000 contiguous bases of nucleotide sequence first disclosed in SEQ ID NO: 1.
2. (Twice Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
 - (a) encodes the amino acid sequence shown in SEQ ID NO: 2; and
 - (b) hybridizes [under highly stringent conditions] to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO: 2.
6. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1.
7. A recombinant expression vector comprising the isolated nucleic acid molecule of claim 1.
8. The recombinant expression vector of claim 7, wherein the isolated nucleic acid molecule encodes the amino acid sequence shown in SEQ ID NO:2.
9. The recombinant expression vector of claim 8, wherein the isolated nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 1.

10. A host cell comprising the recombinant expression vector of claim 7.

Exhibit C

Marked Up Version of Amended Title in U.S. Patent Application Ser. No. 09/818,990

Novel Human Muscle Proteins and Polynucleotides Encoding the Same

Query= SEQ ID NO:1
 (3963 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC024258.9.1.160658	<u>1794</u>	0.0
AL512429.14.1.11170	<u>1159</u>	0.0
AC016395.5.1.166869	<u>442</u>	e-121

>AC024258.9.1.160658
 Length = 160658

Score = 1794 bits (904), Expect = 0.0
 Identities = 904/904 (100%)
 Strand = Plus / Plus

Query: 1 atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat 60
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 Sbjct: 110106 atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat 110165

Query: 61 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110166 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 110225

Query: 121 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110226 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 110285

Query: 181 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 240
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 Sbjct: 110286 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 110345

Query: 241 ctggccatcaattacgaccctttgggagaaggcagatgaaactcaagctagaaaaacgactt 300
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Query: 301 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 360
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 Sbjct: 110406 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 110465

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 Sbjct: 110466 aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat 110525

Query: 421 tgttctgaaacccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 480
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 Sbjct: 110526 tgttctgaaacccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 110585

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Query: 841 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 900
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Sbjct: 110946 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 111005

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||||
Sbjct: 111006 aggt 111009

Score = 728 bits (367), Expect = 0.0
Identities = 372/375 (99%)
Strand = Plus / Plus

Query: 1599 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactcyaccaccaacct 1658
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Query: 1659 ggcagctattgagccacagccctccccaccccaactcagagcctccatctgtggaacaacc 1718
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Sbjct: 155019 ggcagctattgagccacagccctccccaccccaactcagagcctccatctgtggaacaacc 155078

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Sbjct: 155079 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 155138

Query: 1779 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 1838
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Sbjct: 155139 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 155198

Query: 1839 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttscaggagaggttcaa 1898
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Sbjct: 155199 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttccaggagaggttcaa 155258

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Sbjct: 155259 cggacaggcaacaaaaaccccagagccttctttccccggtgaaagagccccctccagttct 155318

Query: 1959 ggccaaaccctaaact 1973
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Score = 355 bits (179), Expect = 1e-94
Identities = 179/179 (100%)
Strand = Plus / Plus

Query: 901 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgtccaggca 960
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Sbjct: 131605 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgtccaggca 131664

Query: 961 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 1020
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Sbjct: 131665 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 131724

Query: 1021 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 1079
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Score = 286 bits (144), Expect = 9e-74
Identities = 144/144 (100%)
Strand = Plus / Plus

Query: 1316 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 1375
|||||
Sbjct: 147151 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 147210

Query: 1376 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 1435
|||||
Sbjct: 147211 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 147270

Query: 1436 cagattttaggattttacagaaaa 1459
|||||
Sbjct: 147271 cagattttaggattttacagaaaa 147294

Score = 238 bits (120), Expect = 2e-59
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1482 agaggagatttgcaccttggtcattgctgaggtgttgcagaagattctgggtgcttcac 1541
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Score = 230 bits (116), Expect = 5e-57
Identities = 116/116 (100%)
Strand = Plus / Plus

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Query: 1190 cagtaccccaagcccagcatttggtggcccaacctcggtggcaaccatccagcag 1245
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Sbjct: 137079 cagtaccccaagcccagcatttggtggcccaacctcggtggcaaccatccagcag 137134

Score = 149 bits (75), Expect = 1e-32
Identities = 75/75 (100%)
Strand = Plus / Plus

Query: 1243 cagtgtcagagccccaccaattacttgcagggattggatggaaaacctatcattgcagct 1302
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Sbjct: 138704 cagtgtcagagccccaccaattacttgcagggattggatggaaaacctatcattgcagct 138763

Query: 1303 cctgtgtttacaaag 1317
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Sbjct: 138764 cctgtgtttacaaag 138778

Score = 107 bits (54), Expect = 5e-20
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1077 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 1130
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Score = 48.1 bits (24), Expect = 0.041
Identities = 24/24 (100%)
Strand = Plus / Plus

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Sbjct: 150396 aacctcgatccatggcagagccag 150419

>AL512429.14.1.11170
Length = 11170

Score = 1159 bits (584), Expect = 0.0
Identities = 588/592 (99%)
Strand = Plus / Plus

Query: 1974 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 2033
|||||
Sbjct: 4075 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 4134

Query: 2034 aaaccacctccttcattctcctaaggagtttctttcarcatgactgttttgaactccaa 2093
|||||
Sbjct: 4135 aaaccacctccttcattctcctaaggagtttctttcagcatgactgttttgaactccaa 4194

Query: 2094 tgctccccccagcggtgacaacatccartaagcaggtgaaggctccttcattcacagacgtt 2153
|||||
Sbjct: 4195 tgctccccccagcggtgacaacatccagtaagcaggtgaaggctccttcattcacagacgtt 4254

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Sbjct: 4255 cagcttggcccgccgaagtatttcttccctccacgaacaccaccgcagcaactgtggc 4314

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|||||
Sbjct: 4435 ttccatccaaaatgagccactcccaccaggcccaacagaacccaacaccaccaccattcac 4494

Query: 2394 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 2453
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Sbjct: 4495 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 4554

Query: 2454 tcctaccagccggattcagaaccagtggtttcctcagctctgttctgccttctctccc 2513
|||||
Sbjct: 4555 tcctaccagccggattcagaaccagtggtttcctcagctctgttctgccttctctccc 4614

Query: 2514 tgccatcccacccacaaatgccatgggrgctgcctagaagtgcaccatccatg 2565
|||||
Sbjct: 4615 tgccatcccacccacaaatgccatggggctgcctagaagtgcaccatccatg 4666

Score = 278 bits (140), Expect = 2e-71
Identities = 140/140 (100%)
Strand = Plus / Plus

Query: 2565 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 2624
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Sbjct: 5332 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 5391

Query: 2625 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 2684
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Sbjct: 5392 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 5451

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>AC016395.5.1.166869
Length = 166869

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Identities = 226/227 (99%)
Strand = Plus / Minus

Query: 2701 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 2760
|||||
Sbjct: 157129 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 157070

Query: 2761 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 2820
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Sbjct: 157069 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 157010

Query: 2821 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 2880
|||||
Sbjct: 157009 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 156950

Query: 2881 ccagtcacattcacctgcaaaattggtgggatacctgttccaaaggt 2927
|||||
Sbjct: 156949 ccagttacattcacctgcaaaattggtgggatacctgttccaaaggt 156903

Score = 417 bits (210), Expect = e-113
Identities = 210/210 (100%)
Strand = Plus / Minus

Query: 3284 aggtgagtgggtttaccgccccggagctgacatggctactcaatggccaacctgtgctac 3343
|||||
Sbjct: 146665 aggtgagtgggtttaccgccccggagctgacatggctactcaatggccaacctgtgctac 146606

Query: 3344 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 3403
|||||
Sbjct: 146605 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 146546

Query: 3404 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 3463
|||||
Sbjct: 146545 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 146486

Query: 3464 attcttttagtctggagctctctgtagtag 3493
|||||
Sbjct: 146485 attcttttagtctggagctctctgtagtag 146456

Score = 339 bits (171), Expect = 6e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

Query: 3793 gctcagtggcaccatcagatcccaccgcccagtgctgtccggcccagtggcagtcgctac 3852
|||||
Sbjct: 135746 gctcagtggcaccatcagatcccaccgcccagtgctgtccggcccagtggcagtcgctac 135687

Query: 3853 ggatctctcaccagtaaaggacttgacatattttctgccttttccatggaaagcacg 3912
|||||
Sbjct: 135686 ggatctctcaccagtaaaggacttgacatattttctgccttttccatggaaagcacg 135627

Query: 3913 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 3963
|||||
Sbjct: 135626 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 135576

Score = 333 bits (168), Expect = 4e-88
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 3492 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 3551
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Sbjct: 144204 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 144145

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|||||
Sbjct: 144084 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 144037

Score = 306 bits (154), Expect = 9e-80
Identities = 158/159 (99%), Gaps = 1/159 (0%)
Strand = Plus / Minus

Query: 2924 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 2983
|||||
Sbjct: 151670 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 151611

Query: 2984 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 3043
|||||
Sbjct: 151610 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 151551

Query: 3044 gcaactacaccatcatggcagccaacccccagg-ggaga 3081
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Sbjct: 151550 gcaactacaccatcatggcagccaacccccagggtggaga 151512

Score = 272 bits (137), Expect = 1e-69
Identities = 137/137 (100%)
Strand = Plus / Minus

Query: 3657 cagtatgcaccaggacacaacaggggtatgcctgccttctcattcagccagccaagaaatc 3716
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Sbjct: 139264 cagtatgcaccaggacacaacaggggtatgcctgccttctcattcagccagccaagaaatc 139205

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Sbjct: 139204 agacgctggatggtacacggtgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 139145

Query: 3777 caggctggatatatacg 3793
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Sbjct: 139144 caggctggatatatacg 139128

Score = 260 bits (131), Expect = 5e-66
Identities = 131/131 (100%)
Strand = Plus / Minus

Query: 3157 aggggaagatccccgagtgcagaaagagacaaagagccccctacaggaacgctttttccga 3216
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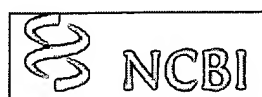
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|||||
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Score = 173 bits (87), Expect = 1e-39
Identities = 87/87 (100%)
Strand = Plus / Minus

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Sbjct: 150524 ctaacctctgctgggtcagtctcacagg 150498



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 CCGCAT
 CACAGAT

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Bio

Search for

Limits

Preview/Index

History

Clipboard

Details

Display

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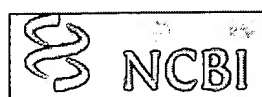
Send to

☐ 1: AC024258. Homo sapiens chro...[gi:20564414]

Links

LOCUS AC024258 160658 bp DNA linear PRI 14-MAY-2002
 DEFINITION Homo sapiens chromosome 10 clone RP11-297N15, complete sequence.
 ACCESSION AC024258
 VERSION AC024258.9 GI:20564414
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 3 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-2001) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 4 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 COMMENT On May 14, 2002 this sequence version replaced gi:16905139.
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[illegible]

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Nucleotide

Protein

Genome

Structure

PMC

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□ **1:** AL512429. Human DNA sequenc...[gi:16508239]

Links

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LOCUS       AL512429             11170 bp      DNA          linear      PRI 26-OCT-2001
DEFINITION  Human DNA sequence from clone RP11-429C3 on chromosome 10, complete
sequence.
ACCESSION   AL512429
VERSION     AL512429.14   GI:16508239
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 11170)
  AUTHORS   Mashreghi-Mohammadi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Oct 29, 2001 this sequence version replaced gi:15028699.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 10, constructed by the Sanger Centre Chromosome 10
            Mapping Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr10
            RP11-429C3 is from the library RPCI-11.2 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            IMPORTANT: This sequence is not the entire insert of clone
            RP11-429C3 It may be shorter because we sequence overlapping
            sections only once, except for a short overlap.
            The true left end of clone RP11-153K11 is at 9171 in this sequence.

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☐ 1: AC016395. Homo sapiens chro...[gi:20564406]

Links

LOCUS AC016395 166869 bp DNA linear PRI 14-MAY-2002
DEFINITION Homo sapiens chromosome 10 clone RP11-153K11, complete sequence.
ACCESSION AC016395
VERSION AC016395.5 GI:20564406
KEYWORDS HTG.
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 3 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 4 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
COMMENT On May 14, 2002 this sequence version replaced gi:9929646.
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Length = 5707

Score = 2649 bits (6790), Expect = 0.0
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Frame = +2

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TECH CENTER 160012900

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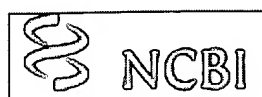
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☐ 1: AF328296. Homo sapiens myop...[gi:13957726]

Links

LOCUS AF328296 5707 bp mRNA linear PRI 06-MAY-2001
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 REFERENCE 1 (bases 1 to 5707)
 AUTHORS Bang, M.L., Mudry, R.E., McElhinny, A.S., Trombitas, K., Geach, A.J.,
 Yamasaki, R., Sorimachi, H., Granzier, H., Gregorio, C.C. and Labeit, S.
 TITLE Myopalladin, a novel 145-kilodalton sarcomeric protein with
 multiple roles in Z-disc and I-band protein assemblies
 JOURNAL J. Cell Biol. 153 (2), 413-427 (2001)
 MEDLINE 21206024
 PUBMED 11309420
 REFERENCE 2 (bases 1 to 5707)
 AUTHORS Bang, M.-L.
 TITLE Direct Submission
 JOURNAL Submitted (13-DEC-2000) Structural and Computational Biology,
 European Molecular Biology Laboratory (EMBL), Meyerhofstrasse 1,
 Heidelberg 69117, Germany
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